

SEQUENCE LISTING



#3

<110> Mitraphanous, Kyrlacos
 Patil, Deva
 Kingsman, Alan
 Kingsman, Susan
 Ellard, Fiona

<120> Retroviral Delivery System

<130> 550-184

<140> 09/701,014

<141> 2000-11-22

<150> PCT/GB99/01607

<151> 1999-05-21

B1
 <150> GB 9811153.7

<151> 1998-07-17

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1650

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: rabies virus strain ERA

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 acatcacctc agctgcccaa acaatttggt agtggaggac gaaggatgca ccaacctgtc 180
 agggttctcc tacatggAAC ttaaagtgg atacatcttA gccataaaaaa tgaacgggtt 240
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 aaccacgttc aaaagaaAGC attcccgccc aacaccagat gcatgttagag ccgcgtacaa 360
 ctggaaatgc gccggtgacc ccagatatga agagtctcta cacaatccgt accctgacta 420
 ccgcgtggctt cgaactgtaa aaaccaccaa ggagtctctc gttatcatat ctccaagtgt 480
 agcagatttgc gaccatatgc acagatccct tcactcgagg gtctcccttA gcggaagtgc 540
 ctcaggagta gcggtgtctt ctacctactg ctccactaac cacgattaca ccatttggat 600
 gccccgagaat ccgagactag ggatgtctt tgacatTTT accaatagta gagggaaagag 660
 agcatccaaa gggagtggAA cttggcggctt tgttagatgaa agaggcctat ataagtctt 720
 aaaaggagca tgcaaactca agttatgtgg agttcttaga cttagactta tggatggAAC 780
 atgggtcgcg atgcaaacat caaatgaaAC caaatggtgc cctcccgatc agttgggtgaa 840
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 caagaccccttA atggaaAGCCG atgctcacta caagtccgtc agaacttggA atgagatcct 1080
 cccttcaaaa ggggtttAA gagttggggg gaggtgtcat cctcatgtga acgggggtgtt 1140
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 cctccctccAG caacatatgg agttgtggA atcctcggtt atcccccttA tgccacccct 1260
 ggcagacccg tctaccgttt tcaaggacgg tgacgaggct gaggattttg ttgaagttca 1320
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gtatgtatta ctgagtgcag gggccctgac tgccttgatg ttgataattt tcctgatgac 1440
atgttgtaga agagtcaatc gatcagaacc tacgcaacac aatctcagag ggacagggag 1500
ggaggtgtca gtcactcccc aaagcgggaa gatcatatct tcatggaat cacacaagag 1560
tgggggttag accagactgt gaggactggc cgtccttca acgatccaag tcctgaagat 1620
cacctccct tggggggttc ttttaaaaaa 1650

<210> 2
<211> 524
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: rabies virus strain ERA

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Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp Lys Leu Gly Pro
20 25 30

Trp Ser Pro Ile Asp Ile His His Leu Ser Cys Pro Asn Asn Leu Val
35 40 45

Val Glu Asp Glu Gly Cys Thr Asn Leu Ser Gly Phe Ser Tyr Met Glu
50 55 60

Leu Lys Val Gly Tyr Ile Leu Ala Ile Lys Met Asn Gly Phe Thr Cys
65 70 75 80

Thr Gly Val Val Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr
85 90 95

Val Thr Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
100 105 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg Tyr Glu
115 120 125

Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp Leu Arg Thr Val
130 135 140

Lys Thr Thr Lys Glu Ser Leu Val Ile Ile Ser Pro Ser Val Ala Asp
145 150 155 160

Leu Asp Pro Tyr Asp Arg Ser Leu His Ser Arg Val Phe Pro Ser Gly
165 170 175

Lys Cys Ser Gly Val Ala Val Ser Ser Thr Tyr Cys Ser Thr Asn His
180 185 190

Asp Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys
195 200 205

Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu
210 215 220

B
D
920402-112200

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu Lys Gly
225 230 235 240

Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu Arg Leu Met Asp
245 250 255

Gly Thr Trp Val Ala Met Gln Thr Ser Asn Glu Thr Lys Trp Cys Pro
260 265 270

Pro Asp Gln Leu Val Asn Leu His Asp Phe Arg Ser Asp Glu Ile Glu
275 280 285

His Leu Val Val Glu Glu Leu Val Arg Lys Arg Glu Glu Cys Leu Asp
290 295 300

Ala Leu Glu Ser Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu
305 310 315 320

Ser His Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
325 330 335

Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser Val Arg
340 345 350

Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu Arg Val Gly Gly
355 360 365

Arg Cys His Pro His Val Asn Gly Val Phe Phe Asn Gly Ile Ile Leu
370 375 380

Gly Pro Asp Gly Asn Val Leu Ile Pro Glu Met Gln Ser Ser Leu Leu
385 390 395 400

Gln Gln His Met Glu Leu Leu Glu Ser Ser Val Ile Pro Leu Val His
405 410 415

Pro Leu Ala Asp Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu
420 425 430

Asp Phe Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly
435 440 445

Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu Ser Ala
450 455 460

Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys
465 470 475 480

Arg Arg Val Asn Arg Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr
485 490 495

Gly Arg Glu Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser
500 505 510

Trp Glu Ser His Lys Ser Gly Gly Glu Thr Arg Leu
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Sequence*

<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 4
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 4
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